IN THE CLAIMS:

Please cancel claims 1 - 58 without prejudice.

Please add the following new claims 59 to 130:

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59 (newly added). A method of selling and/or licensing single-exon microarrays to a customer, the method comprising:

making available for computerized query a database having a plurality of records, each record identifying a single exon microarray;

responding to a customer query of the database by returning to the customer at least one record, or an identifier of the at least one record, that identifies at least one microarray that is responsive to the customer query; and

offering for sale and/or license to the querying customer each of the at least one single exon microarrays identified in the at least one record,

wherein at least 50% of the probes addressably disposed on each of said at least one microarray are single exon probes that include a fragment of no more than one exon of a eukaryotic genome, said fragment selectively hybridizable at high stringency to an expressed gene, wherein said plurality of nucleic acid probes averages at least 100 bp in length, and wherein said eukaryotic genome averages at least one intron per gene.

60 (newly added). The method of claim 59, wherein at least 95% of the nucleic acid probes addressably disposed on each of said at least one microarrays includes a selectively

hybridizable portion of no more than one exon of said eukaryotic genome.

61 (newly added). The method of claim 59, wherein at least 50% of the single exon nucleic acid probes addressably disposed on each of said at least one microarrays further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

62 (newly added). The method of claim 59, wherein at least 95% of said single exon nucleic acid probes addressably disposed on each of said at least one microarrays further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

63 (newly added). The method of claim 59, wherein at least 50% of said single exon nucleic acid probes addressably disposed on each of said at least one microarrays further comprise, (i) contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome, and (ii) contiguous to a second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

64 (newly added). The method of claim 59, wherein at least 95% of said single exon nucleic acid probes

addressably disposed on each of said at least one microarrays further comprise, (i) contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome, and (ii) contiguous to a second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

65 (newly added). The method of claim 59, wherein at least 50% of said single exon nucleic acid probes addressably disposed on each of said at least one microarrays lack prokaryotic and bacteriophage vector sequence.

66 (newly added). The method of claim 59, wherein at least 95% of said single exon nucleic acid probes addressably disposed on each of said at least one microarrays lack prokaryotic and bacteriophage vector sequence.

67 (newly added). The method of claim 59, wherein at least 50% of said single exon nucleic acid probes addressably disposed on each of said at least one microarrays lack homopolymeric stretches of A or T.

68 (newly added). The method of claim 59, wherein at least 95% of said single exon nucleic acid probes addressably disposed on each of said at least one microarrays lack homopolymeric stretches of A or T.

69 (newly added). The method of claim 59, wherein said eukaryotic genome averages at least two introns per gene.

70 (newly added). The method of claim 59, wherein said eukaryotic genome averages at least three introns per gene.

71 (newly added). The method of claim 59, wherein said eukaryotic genome averages at least five introns per gene.

72 (newly added). The method of claim 59, wherein said genome is a human genome.

73 (newly added). The method of claim 59, wherein said steps of responding to customer query and offering for sale and/or license to the querying customer are performed by a digital computer.

74 (newly added). The method of claim 73, wherein each of said addressably disposed single exon probes comprises a nucleotide sequence selected from the group consisting of exon SEQ ID NOs: set forth in Tables 4, 5, 6, 7, 8, 9, 10, 11, 12, and 13, and the complements thereof, and each of said single exon probes hybridizes under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues.

75 (newly added). The method of claim 74, wherein each of the single exon probes of at least one of said at least

one microarrays comprises a nucleotide sequence selected from the group consisting of exon SEQ ID NOs: set forth in Table 5.

76 (newly added). The method of claim 74, wherein said at least one microarray comprises at least a first single exon probe that includes SEQ ID NO:17240 and a second single exon probe that includes SEQ ID NO:17651.

77 (newly added). The method of claim 76, wherein said at least one microarray is offered for sale.

78 (newly added). The method of claim 77, wherein said at least one microarray is offered for license.

79 (newly added). A method of selling and/or licensing single exon probes to a customer, the method comprising:

making available for computerized query a database having a plurality of records, each record identifying a single exon probe;

responding to a customer query of the database by returning to the customer at least one record, or an identifier of the at least one record, that identifies at least one single exon probe that is responsive to the customer query; and

offering for sale and/or license to the querying customer each of the at least one single exon probes identified in the at least one record,

wherein each of said offered single exon probes averages at least 100 bp in length, includes a fragment of no

more than one exon of a eukaryotic genome, said fragment selectively hybridizable at high stringency to an expressed gene, and wherein said eukaryotic genome averages at least one intron per gene.

80 (newly added). The method of claim 79, wherein at least 50% of said offered single exon probes further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

81 (newly added). The method of claim 79, wherein at least 50% of said offered single exon probes further comprise, (i) contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome, and (ii) contiguous to a second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

82 (newly added). The method of claim 79, wherein at least 50% of said offered single exon nucleic acid probes lacks prokaryotic and bacteriophage vector sequence.

83 (newly added). The method of claim 79, wherein at least 50% of said offered single exon nucleic acid probes lacks homopolymeric stretches of A or T.

84 (newly added). The method of claim 79, wherein said eukaryotic genome averages at least two introns per gene.

85 (newly added). The method of claim 79, wherein said eukaryotic genome averages at least three introns per gene.

86 (newly added). The method of claim 79, wherein said eukaryotic genome averages at least five introns per gene.

87 (newly added). The method of claim 79, wherein said genome is a human genome.

88 (newly added). The method of claim 79, wherein said steps of responding to customer query and offering for sale and/or license to the querying customer are performed by a digital computer.

89 (newly added). The method of claim 88, wherein each of said offered single exon probes comprises a nucleotide sequence selected from the group consisting of exon SEQ ID NOs: set forth in Tables 4, 5, 6, 7, 8, 9, 10, 11, 12, and 13, and the complements thereof, and each of said single exon probes hybridizes under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues.

90 (newly added). The method of claim 89, wherein each of said offered single exon probes comprises a nucleotide

sequence selected from the group consisting of exon SEQ ID NOs: set forth in Table 5.

91 (newly added). The method of claim 90, wherein at least one of said offered single exon probes comprises the nucleotide sequence of exon SEQ ID NO: NO:17240.

92 (newly added). The method of claim 91, wherein said at least one single exon probe is offered for sale.

93 (newly added). The method of claim 91, wherein said at least one single exon probe is offered for license.

94 (newly added). A method of providing human gene expression data by subscription, comprising:

making available for computerized query a database having a plurality of records, each record including data on the expression of one single exon probe;

responding to a query of said database, when received from a customer having a subscription to said database, by returning at least one record, or identifier of said at least one record, that includes expression data for a single exon probe responsive to said query,

wherein each of the single exon probes responsive to said subscription customer query averages at least 100 bp in length, includes a fragment of no more than one exon of a eukaryotic genome, said fragment selectively hybridizable at high stringency to an expressed gene, and wherein said eukaryotic genome averages at least one intron per gene.

95 (newly added). The method of claim 94, wherein at least 50% of said responsive single exon probes further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

96 (newly added). The method of claim 94, wherein at least 50% of said responsive single exon probes further comprise, (i) contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome, and (ii) contiguous to a second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

97 (newly added). The method of claim 94, wherein at least 50% of said responsive single exon nucleic acid probes lacks prokaryotic and bacteriophage vector sequence.

98 (newly added). The method of claim 94, wherein at least 50% of said responsive single exon nucleic acid probes lacks homopolymeric stretches of A or T.

99 (newly added). The method of claim 94, wherein said eukaryotic genome averages at least two introns per gene.

100 (newly added). The method of claim 94, wherein said eukaryotic genome averages at least three introns per gene.

101 (newly added). The method of claim 94, wherein said eukaryotic genome averages at least five introns per gene.

102 (newly added). The method of claim 94, wherein said genome is a human genome.

103 (newly added). The method of claim 94, wherein said step of responding to customer query is performed by a digital computer.

104 (newly added). The method of claim 103, wherein each of said responsive single exon probes comprises a nucleotide sequence selected from the group consisting of exon SEQ ID NOs: set forth in Tables 4, 5, 6, 7, 8, 9, 10, 11, 12, and 13, and the complements thereof, and each of said single exon probes hybridizes under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues.

105 (newly added). The method of claim 104, wherein each of said responsive single exon probes comprises a nucleotide sequence selected from the group consisting of exon SEQ ID NOs: set forth in Table 5.

106 (newly added). The method of claim 105, wherein at least one of said responsive single exon probes comprises the nucleotide sequence of exon SEQ ID NO:17240.

107 (newly added). The method of claim 105, further comprising the step of:

offering said single exon probe for sale and/or license.

108 (newly added). The method of claim 107, wherein said single exon probe is offered for sale.

109 (newly added). The method of claim 107, wherein said single exon probe is offered for license.

110 (newly added). A method of manufacturing a microarray that has single exon probes that share at least one customer-identified attribute in common, comprising:

receiving data from a customer that identify at least one desired common probe attribute;

identifying within a database a plurality of single exon probes having the customer-desired probe attribute; and then

addressably disposing said identified probes on a support substrate capable of functioning in microarray hybridization experiments,

wherein at least 50% of the probes addressably disposed on said microarray are single exon probes that include a fragment of no more than one exon of a eukaryotic genome,

said fragment selectively hybridizable at high stringency to an expressed gene, wherein said plurality of nucleic acid probes averages at least 100 bp in length, and wherein said eukaryotic genome averages at least one intron per gene.

111 (newly added). The method of claim 110, wherein at least 95% of the nucleic acid probes addressably disposed on said microarray include a selectively hybridizable portion of no more than one exon of said eukaryotic genome.

112 (newly added). The method of claim 110, wherein at least 50% of the single exon nucleic acid probes addressably disposed on said microarray further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

113 (newly added). The method of claim 110, wherein at least 95% of said single exon nucleic acid probes addressably disposed on said microarray further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

114 (newly added). The method of claim 110, wherein at least 50% of said single exon nucleic acid probes addressably disposed said microarray further comprise, (i) contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically

contiguous to said fragment in the human genome, and (ii) contiguous to a second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

115 (newly added). The method of claim 110, wherein at least 95% of said single exon nucleic acid probes addressably disposed said microarray further comprise, (i) contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome, and (ii) contiguous to a second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

116 (newly added). The method of claim 110, wherein at least 50% of said single exon nucleic acid probes addressably disposed said microarray lack prokaryotic and bacteriophage vector sequence.

117 (newly added). The method of claim 110, wherein at least 95% of said single exon nucleic acid probes addressably disposed said microarray lack prokaryotic and bacteriophage vector sequence.

118 (newly added). The method of claim 110, wherein at least 50% of said single exon nucleic acid probes addressably disposed said microarray lack homopolymeric stretches of A or T.

119 (newly added). The method of claim 110, wherein at least 95% of said single exon nucleic acid probes addressably disposed said microarray lack homopolymeric stretches of A or T.

120 (newly added). The method of claim 110, wherein said eukaryotic genome averages at least two introns per gene.

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121 (newly added). The method of claim 110, wherein said eukaryotic genome averages at least three introns per gene.

122 (newly added). The method of claim 110, wherein said eukaryotic genome averages at least five introns per gene.

123 (newly added). The method of claim 110, wherein said genome is a human genome.

124 (newly added). The method of claim 110, wherein said steps of receiving customer data and identifying within a database are performed by a digital computer.

125 (newly added). The method of claim 124, wherein each of said addressably disposed single exon probes comprises a nucleotide sequence selected from the group consisting of exon SEQ ID NOs: set forth in Tables 4, 5, 6, 7, 8, 9, 10, 11, 12, and 13, and the complements thereof, and each of said

single exon probes hybridizes under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues.

126 (newly added). The method of claim 125, wherein each of said addressably disposed single exon probes comprises a nucleotide sequence selected from the group consisting of exon SEQ ID NOs: set forth in Table 5.

127 (newly added). The method of claim 126, wherein said microarray comprises at least a first single exon probe that includes SEQ ID NO:17240 and second single exon probe that includes SEQ ID NO:17651.

128 (newly added). The method of claim 127, further comprising offering said microarray for sale and/or license.

129 (newly added). The method of claim 128, wherein said microarray is offered for sale.

130 (newly added). The method of claim 128, wherein said microarray is offered for license.

REMARKS

In response to the requirements for restriction and election of species, applicants elect without traverse to prosecute the invention of: